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FIG. 1

1 CCG CTC ACA TTG GGA TTC GTC ATT CTT CTT CTA AAA CCC GCA AAA TTT CTC CAT TTC TAC
 61 CAA AAA TAT CCA ACT TTT ACT TTT CTT TCC TGT GAA ATT ATC TGC TCA AAT CTT TGG TTC
 121 CTG ACG GAG ATG GCG GCG ATT TCA GGC ATC TCC TCT GGT ACG TIG ACG ATT TCA CGG CCT
 M A A I S G I S S G T L T I S R P
 181 TTG GTT ACT CTT CGA CGC TCT AGA GCC GCC GTT TCG TAC AGC TCC TCT CAC CGA TTG CTT
 L V T L R R S R A A V S Y S S S H R L L
 241 CAT CAT CTT CCT CTC TCT CGT CGT CTG CTA TTA AGG AAC AAT CAT CGA GTC CAA CGA
 H H L P L S S R R L L R N N H R V Q * A
 301 ACG ATT TTG CAA GAC GAT GAA GAG AAA GTG GTG GTG GAG GAA TCG TTT AAA GCC GAG ACT
 T I L Q D D E E K V V V E E S F K A E T
 361 TCT ACT GGT ACA GAA CCA CTT GAG GAG CCA AAT ATG AGT TCT TCT TCA ACT AGT GCT TTT
 S T G T E P L E E P N M S S S S T S A F
 421 GAG ACA TGG ATC ATC AAG CTT GAG CAA GGA GTG AAT GTT TTC CTT ACA GAC TCG GTT ATT
 E T W I I K L E Q G V N V F L T D S V I
 481 AAG ATA CTT GAC ACT TTG TAT CGT GAC CGA AGA TAT GCA AGG TTC TTT GTT CTT GAG ACA
 K I L D T L Y R D R T Y A R F F V L E T
 541 ATT GCT AGA GTG CCT TAT TTT GCG TTT ATG TCT GTG CTA CAT ATG TAT GAG ACC TTT GGT
 I A R V P Y F A F M S V L H M Y E T F G
 601 TGG TGG AGG AGA GCA GAT TAT TTG AAA GTA CAC TTT GCT GAG AGC TGG AAT GAA ATG CAT
 W W R R A D Y L K V H F A E S W N E M H
 661 CAC TTG CTC ATA ATG GAA GAA TTG GGT GGA AAT TCT TGG TGG TTT GAT CGT TTT CTG GCT
 H L L I M E E L G G N S W W F D R F L A
 721 CAG CAC ATA GCA ACC TTC TAC TAC TTC ATG ACA GTG TTC TTG TAT ATC TTA AGC CCT AGA
 Q H I A T F Y Y F M T V F L Y I L S P R
 781 ATG GCA TAT CAC TTT TCG GAA TGT GTG GAG AGT CAT GCA TAT GAG ACT TAT GAT AAA TTT
 M A Y H F S E C V E S H A Y E T Y D K F
 841 CTC AAG GCC AGT GGA GAG GAG TTG AAG AAT ATG CCT GCA CCG GAT ATC GCA GTC AAA TAC
 L K A S G E E L K N M P A P D I A V K Y
 901 TAT ACG GGA GGT GAC TTG TAC TTA TTT GAT GAG TTC CAA ACA TCA AGA ACT CCC AAT ACT
 Y T G G D L Y L F D E F Q T S R T P N T
 961 CGA AGA CCA GTC ATA GAA AAT CTA TAC GAT GTG TTT GTG AAC ATA AGA GAT GAT GAA GCA
 R R P V I E N L Y D V F V N I R D D E A
 1021 GAA CAC TGC AAG ACA ATG AGA GCT TGT CAG ACT CTA GGC AGT CTG CGT TCT CCA CAC TCC
 E H C K T M R A C Q T L G S L R S P H S
 1081 ATT TTA GAT GAT GAT GAT ACT GAA GAA GAA TCA GGG TGT GTT GTT CCT GAG GAG GCT CAT
 I L D D D D T E E E S G C V V P E E A H
 1141 TGC GAA GGT ATT GTA GAC TGC CTC AAG AAA TCC ATT ACA AGT TAA TAA ATT AGA AAG TAA
 C E G I V D C L K K S I T S
 1201 ACT AAA AAA GAT TAT TTG TAT CAG CTC ATG AAC AAT AGA TAT AAT CCC ATA TAC TTG GGA
 1261 ATA AAG GAA TAA TGT GAA ATT CCC ATC GTT GTG CTA GTG TGT GAG AGA ATC AAA TAC CCT
 1321 AAT GAT GTA AAT GTA CTT TGA TGA CCT TAA GTC GTT GTA GAC CAT TTT ATC AAA AAA AAA
 1381 AAA AAA AAA AAA AAA A

FIG. 2

IMM	:	111	FLTDSVIKILLDTLYRDRTYA-R	RE	YVTEETE	TATPXTATMSV	EMYET	FGWRRADYLKVHF	169		
		+ T	+++I	L+	R	Y	R	+LET+A VP			
								+ LH+	+	+	++K
AOX	:	136	YRTVKLLRIPTDLFFKRRYGCRA	MME	TEVNA	PGM	CHM	ELRSLRKFQQSGGWIKALL	195		
IMM	:	170	AESWNEMHLLLIMEELGGNSWWFDR	ELAQH	YNE	YEN	VEN	PRMAYHFSECVESH	229		
		E+	NE	HL+	M EL	W++R	L	++	LYLSP+ +A+	+E	
AOX	:	196	EEAENERMHLMTMVEL-VKPKWYER	TIVTA	AVOC	VEEN	YKZ	SPKVAHRIVGYLEEEE	254		
IMM	:	230	AYETYDKFLK-ASGEELKNMPAPDIAVKKYYTGGDLYLFDEFQTSRTPNTRPVITENLYDV	288							
		A	+ Y	++LK		++N+PAP	IA+ Y+				
AOX	:	255	AIHSYSTEYLKDLESGAENVPAAPAIDYW	-----	-----	-----	-----	-RLPKDARLKDV	295		
IMM	:	289	FVNIRDDEAEH	299							
			IR DEA H								
AOX	:	296	ITVIRADEAHH	306							

FIG. 3A

T 1 MAISISAMSFGTSVSSYSCFRARSFEKSSVLCNSQNPCRFNSVFP.IRKSDGASRCCSVSR
 P 1 MAISISAMSFRTSVSS.....SY..SAFLCNSKNPFCLNSLFS.LRNSHRTFQPSLSR
 A 1 MA.AISGISSGTLTIS.....RPLVTLRRSRAAVSYSSSHRLLHHPLSSRLLL
 consensus

1 MA	ISams	T	S	L	S	S	lr	1 R
------	-------	---	---	---	---	---	----	-----

T 60 KSCRVRATLLQENEVEVVEKSFAPKSFPDNVGGSNGKPPDDSSS.NGLEKWVIKLEQS
 P 51 KSSRVATLLKENEEVEVVEKSFAPKSFPGNVGNNNGEPPDNSSS.NGLEKWVIKIEQS
 A 51 NNHRVQATILQDDEEKVVVEESFKAE...TSTGTEPLEEPNMSSSSTAFETWIICKLEQG
 consensus

61	RV	AT1L	e	EE	VVVE	SF	G	P	SSS	g	E	WvIKIEQ
----	----	------	---	----	------	----	---	---	-----	---	---	---------

T 119 VNILLTDSEVIKILDLYHNRNYARFFVLETIARVPYFAFISVLHMYESFGWWRRADYMKV
 P 110 VNIFLTDSVIKILDLYHDRHYARFFVLETIARVPYFAFISVLHLYESFGWWRRADYLKV
 A 108 VNVFLTDSEVIKILDLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWWRRADYLKV
 consensus

121 VNI LTDSVIKILDLYh R YARFFVLETIARVPYFAFISVLHLYEFGWWRRADY1KV

T 179 HFAESWNEMHLLIMEELGGNAWWFDRFLAQHIAIFYYFMTVLMYALSPRMAYHFSECVE
 P 170 HFAESWNEMHLLIMEELGGNAWWFDRFLAQHIAVFYYFMTVSMYALSPRMAYHFSECVE
 A 168 HFAESWNEMHLLIMEELGGNSWWFDRFLAQHIATFYFMTVFLYILSPRMAYHFSECVE
 Consensus

181 HFAESWNEMHLLIMEELGGN WWFDRFLAQHIA FYYFMTV mY LSPRMAYHFSECVE

T 239 SHAYETYDKFIKDQGEELKNLPAPKIAVDYYTGGDLYLFDEFQTSREPNTRRPKIDNLYD
 P 230 HHAYETYDKFIKDQEAELKKLPAPKIAVSYYTGGDLYLFDEFQTSREPNTRRPKIDNLYD
 A 228 SHAYETYDKFLKASGEELKNMPAPDIAVKYYTGGDLYLFDEFQTSRTPNTRRPVIENLYD
 Consensus

241 HAYETYDKFIK ELK 1PAP IAV YYTGGDLYLFDEFQTSR PNTRRP IdNLYD

T 299 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTD.PCDDSEDDTGCSVP.QADCIGIVDCIKK
 P 290 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTN.PCDESEDDPGCSVP.QADCVGIVDCITK
 A 288 VFVNIRDDEAEHCKTMRACQTLGSLRSPHSILDDDDTEESGCVPEAHCEGIVDCLKK
 Consensus

301 VFMNIRDDEAEHCKTMKACQT GSLRSPHT DdsEd GC VP A C GIVDCI K

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FIG. 3B

T 357 SVTDTQVTKR

P 348 SVADPNVGRR

A 348 SITS.....

Consensus

361 Sv

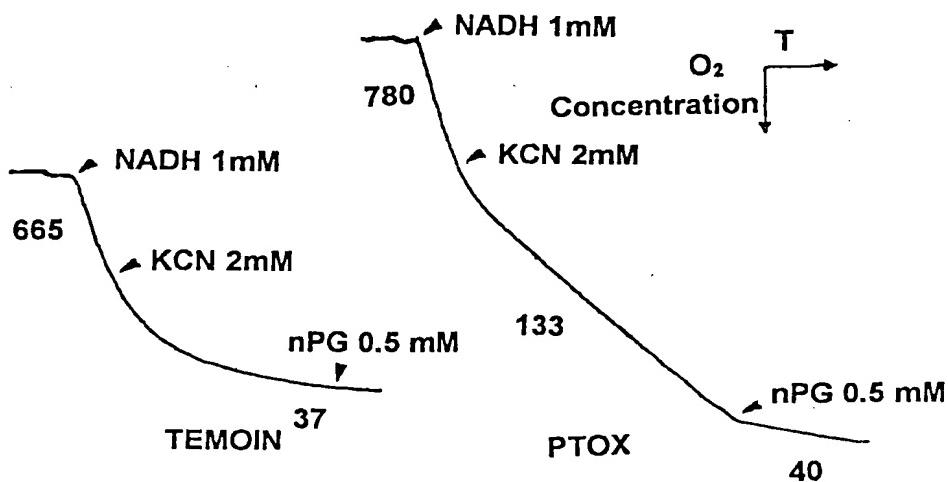


FIG. 4A

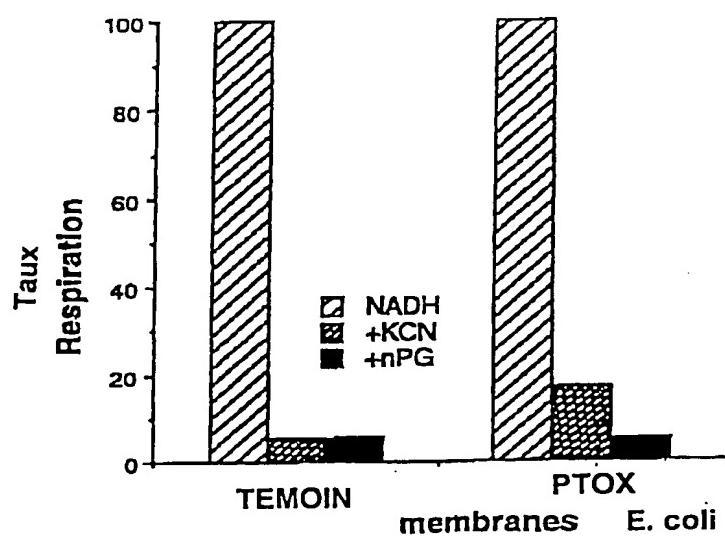


FIG. 4B